

Substitute for form 1449A/PTO

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Application Number

Filing Date

August 26, 2003

First Named Inventor

Pramod B. Mahajan

Art Unit

Examiner Name

Attorney Docket Number

1264C

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Examiner Initials*	Cite No. ¹	Foreign Patent Document	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T ⁶
		Country Code ³ - Number ⁴ - Kind Code ⁵ (if known)				
↓	A2	WO 00/42205 A2	07/20/2000	Novartis-Erfindungen	Whole Document	
	A3	WO 00/12716 A2	03/09/2000	Pioneer Hi-Bred	Whole Document	
	A4	WO 99/41394 A1	08/19/1999	Pioneer Hi-Bred	Whole Document	
	A5	WO 97/08331 A1	03/06/1997	Max-Planck-Gesellschaft	Whole Document	
	A6	WO 00/15816 A3	03/23/2000	Pioneer Hi-Bred	Whole Document	
	A7	WO 99/37789 A1	07/29/1999	Pioneer Hi-Bred	Whole Document	

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**INFORMATION DISCLOSURE
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Group Art Unit	
Examiner Name	
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OTHER PRIOR ART -- NON PATENT LITERATURE DOCUMENTS

Examiner Initials *	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T ²
BB	A8	CHAMANKHAH et al., Isolation of hMRE11B: failure to complement yeast mre11 defects due to species-specific protein interactions, Gene 225:107-116 (1998)	
	A9	TAVASSOLI et al., Cloning and characterisation of the Schizosaccharomyces pombe rad32 gene: a gen required for repair of double strand breaks and recombination, Nucleic Acids Res. 23(3):383-388 (1995)	
	A10	USUI et al., Complex Formation and Functional Versatility of Mre11 Budding Yeast in Recombination, Cell 95:705-716 (1998)	
	A11	LEE et al., Saccharomyces Ku70, Mre11/Rad50 and RPA Proteins Regulate Adaptation to G2/M Arrest after DNA Damage, Cell 94:399-409 (1998)	
	A12	CARNEY et al., The hMre11/hRad50 Protein Complex and Nijmegen Breakage Syndrome: Linkage of Double-Strand Break Repair to the Cellular DNA Damage Response: Cell 93:477-486 (1998)	
	A13	TSUKAMOTO et al., Effects of Mutations of RAD50, RAD51, RAD52, and Related Genes on Illegitimate Recombination in Saccharomyces cerevisiae, Genetics 142:383-391 (1996)	
	A14	PAULL et al., The 3' to 5' Exonuclease Activity of Mre11 Facilitates Repair of DNA Double-Strand Breaks, Molecular Cell 1:969-979 (1998)	
	A15	TRUJILLO et al., Nuclease Activities in a Complex of Human Recombination and DNA Repair Factors Rad50, Mre11, and p95, J. Biol. Chem. 273(34):21447-21450 (1998)	
	A16	AJIMURA et al., Identification of New Genes Required for Meiotic Recombination in Saccharomyces cerevisiae, Genetics 133:51-66 (1993)	
	A17	JOHZUKA et al., Interaction of Mre11 and Rad50: Two Proteins Required for DNA Repair and Meiosis-Specific Double-Strand Break Formation in Saccharomyces cerevisiae, Genetics 139:1521-1532 (1995)	
✓	A18	PETRINI et al., Isolation and Characterization of the Human MRE11 Homologue, Genomics 29:80-86 (1995)	

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BB	A19	FURUSE et al., Distinct roles of two separable in vitro activities of yeast Mre11 in mitotic and meiotic recombination, EMBO Journal 17(21):6412-6425 (1998)	
	A20	XIAO et al., Conditional gene targeted deletion by Cre recombinase demonstrates the requirement for the double-strand break repair Mre11 protein in murine embryonic stem cells, Nucleic Acids Res. 25(15):2985-2991 (1997)	
	A21	YAMAGUCHI-IMAI et al., Mre11 is essential for the maintenance of chromosomal DNA in vertebrate cells, EMBO Journal 18(23):6619-6629 (1999)	
	A22	WILSON et al., The role of Schizosaccharomyces pombe Rad32, the Mre11 homologue, and other DNA damage response proteins in non-homologous end joining and telomere length maintenance, Nucleic Acids Res. 27(13):2655-2661 (1999)	
	A23	DOLGANOV et al., Human Rad50 is Physically Associated with Human Mre11: Identification of a Conserved Multiprotein Complex Implicated in Recombinational DNA Repair, Mol. Cell. Biol. 16(9):4832-4841 (1996)	
	A24	LEWIS et al., Repair of Endonuclease-Induced Double-Strand Breaks in Saccharomyces cerevisiae: Essential Role for Genes Associated with Nonhomologous End-Joining, Genetics 152:1513-1539 (1999)	
	A25	MOORE et al., Cell Cycle and Genetic Requirements of Two Pathways of Nonhomologous End-Joining Repair of Double-Strand Breaks in Saccharomyces cerevisiae, Mol. Cell Biol. 16(5):2164-2173 (1996)	
	A26	NAIRZ et al., mre11S-yeast mutation that blocks double-strand-break processing and permits nonhomologous synapsis in meiosis, Genes & Development 11:2272-2290 (1997)	
	A27	TSUBOUCHI et al., A Novel mre11 Mutation Impairs Processing of Double-Strand Breaks of DNA during Both Mitosis and Meiosis, Mol. Cell. Biol. 18(1):260-268 (1998)	
	A28	HARTUNG et al., Accession No. Q9XGM2, Arabidopsis thaliana (Mouse-ear cress), (1999)	
	A29	HARTUNG et al., Accession No. AJ243822, Arabidopsis thaliana mRNA for Mre11 protein (MRE11 gene), (1999)	

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First Named Inventor

Pramod B. Mahajan

Group Art Unit

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BB	A30	GERECKE et al., Accession No. AF178433, Coprinus cinereus DNA repair and meiosis protein Mre11 (mre11) gene, complete cds (1999)	
	A31	BIBIKOVA et al., Accession No. AF134569, Xenopus laevis putative nuclease Mre11 (MRE11) mRNA, complete cds (1999)	
	A32	BRODSKY et al., Accession No. AF132144, Drosophila melanogaster clone LD8638 endo/exonuclease Mre11 (mre11) mRNA, complete cds (1999)	
	A33	HARTUNG et al., Isolation of the Complete cDNA of the Mre11 Homologue of Arabidopsis (Accession No. AJ243822) Indicated Conservation of DNA Recombination Mechanisms Between Plants and Other Eucaryotes, Plant Gene Register PGR99-132 Plant Physiol. 121:132 (1999)	
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	A35	JAESUNG et al., Accession No. PREV199800510932, Agrobacterium tumefaciens transformation of the thaliana mutants uvh1 and rad5 (1998)	
	A36	NAM et al., Agrobacterium tumefaciens Transformation of the Radiation Hypersensitive Arabidopsis thaliana Mutants uvh1 and rad5, MPML 11(11):1136-1141 (1998)	
	A37	MYSORE et al., An arabidopsis histone H2A mutant is deficient in Agrobacterim T-DNA integration, PNAS 97(2):948-953 (2000)	
	A38	LEWIN, B., Most eukaryotic mRNAs are polyadenylated at the 3' end, Genes V 10:264-165 (1994), Oxford University Press, New York	
	A39	DOERKS, T., Protein annotation: detective work for function prediction, TIG 14(6):248-250 (1998)	
✓	A40	SMITH et al., The challenges of genome sequence annotation or "The devil is in the details", Nature Biotechnology 15:1222-1223 (1997)	

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Sheet 5 of 5	Attorney Docket Number	1264C	

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BB ↓	A41	BRENNER, S.E., Errors in genome annotation, TIG 15(4):132-133 (1999)	
	A42	BORK et al., Go hunting in sequence databases but watch out for the traps, TIG 12(10):425-427 (1996)	
	A43	VAN DE LOO et al., An oleate 12-hydroxylase from Ricinus communis L. is a fatty acyl desaturase homolog, Proc. Natl. Acad. Sci. USA 92:6743-6747 (1995)	

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